RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _08/910, 449_

Source: _IFW16_

Date Processed by STIC: _07/18/2006_

ENTERED

IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/08/910,449**

DATE: 07/18/2006
TIME: 10:52:33

Input Set : **N:\Crf3\RULE60\08910449.RAW**
Output Set: **N:\CRF4\07172006\H910449.raw**

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Alderson, Mark R.
6   Goodwin, Raymond G.
7   Smith, Craig A.
9   (ii) TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
11   (iii) NUMBER OF SEQUENCES: 18
13   (iv) CORRESPONDENCE ADDRESS:
14   (A) ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
15   (B) STREET: 51 University Street
16   (C) CITY: Seattle
17   (D) STATE: Washington
18   (E) COUNTRY: US
19   (F) ZIP: 98101
21   (v) COMPUTER READABLE FORM:
22   (A) MEDIUM TYPE: Floppy disk
23   (B) COMPUTER: Apple Power Macintosh
24   (C) OPERATING SYSTEM: Apple 7.5.3
25   (D) SOFTWARE: Microsoft Word, Version #6.0.1
27   (vi) CURRENT APPLICATION DATA:
C--> 28   **(A) APPLICATION NUMBER: US/08/910,449**
C--> 29   **(B) FILING DATE: 05-Aug-1997**
W--> 39   **(C) CLASSIFICATION: 435**
32   (vii) PRIOR APPLICATION DATA:
33   (A) APPLICATION NUMBER: US/08/236,918
34   (B) FILING DATE: 06-May-1994
37   (A) APPLICATION NUMBER: US 08/060,843
38   (B) FILING DATE: 07-May-1993
42   (viii) ATTORNEY/AGENT INFORMATION:
43   (A) NAME: Anderson, Kathryn A.
44   (B) REGISTRATION NUMBER: 32,172
45   (C) REFERENCE/DOCKET NUMBER: 2801-B
47   (ix) TELECOMMUNICATION INFORMATION:
48   (A) TELEPHONE: (206) 587-0430
49   (B) TELEFAX: (206) 233-0644
52 (2) INFORMATION FOR SEQ ID NO: 1:
54   (i) SEQUENCE CHARACTERISTICS:
55   (A) LENGTH: 1254 base pairs
56   (B) TYPE: nucleic acid
57   (C) STRANDEDNESS: single
58   (D) TOPOLOGY: linear
60   (ii) MOLECULE TYPE: cDNA to mRNA
62   (iii) HYPOTHETICAL: NO

RAW SEQUENCE LISTING   DATE: 07/18/2006
PATENT APPLICATION: US/08/910,449 TIME: 10:52:33

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Output Set: N:\CRF4\07172006\H910449.raw

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64      (iv) ANTI-SENSE: NO
67     (vii) IMMEDIATE SOURCE:
68          (B) CLONE: murine 4-1BB-L
70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 53..979
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77  AGCCTATAAA GCACGGGCAC TGGCGGGAGA CGTGCACTGA CCGACCGTGG TA ATG         55
78                                                              Met
79                                                               1
81  GAC CAG CAC ACA CTT GAT GTG GAG GAT ACC GCG GAT GCC AGA CAT CCA      103
82  Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro
83               5                  10                  15
85  GCA GGT ACT TCG TGC CCC TCG GAT GCG GCG CTC CTC AGA GAT ACC GGG      151
86  Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly
87              20                  25                  30
89  CTC CTC GCG GAC GCT GCG CTC CTC TCA GAT ACT GTG CGC CCC ACA AAT      199
90  Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn
91         35                  40                  45
93  GCC GCG CTC CCC ACG GAT GCT GCC TAC CCT GCG GTT AAT GTT CGG GAT      247
94  Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp
95  50                  55                  60                  65
97  CGC GAG GCC GCG TGG CCG CCT GCA CTG AAC TTC TGT TCC CGC CAC CCA      295
98  Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro
99                      70                  75                  80
101 AAG CTC TAT GGC CTA GTC GCT TTG GTT TTG CTG CTT CTG ATC GCC GCC      343
102 Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala Ala
103                 85                  90                  95
105 TGT GTT CCT ATC TTC ACC CGC ACC GAG CCT CGG CCA GCG CTC ACA ATC      391
106 Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile
107             100                 105                 110
109 ACC ACC TCG CCC AAC CTG GGT ACC CGA GAG AAT AAT GCA GAC CAG GTC      439
110 Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val
111         115                 120                 125
113 ACC CCT GTT TCC CAC ATT GGC TGC CCC AAC ACT ACA CAA CAG GGC TCT      487
114 Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser
115 130                 135                 140                 145
117 CCT GTG TTC GCC AAG CTA CTG GCT AAA AAC CAA GCA TCG TTG TGC AAT      535
118 Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn
119                 150                 155                 160
121 ACA ACT CTG AAC TGG CAC AGC CAA GAT GGA GCT GGG AGC TCA TAC CTA      583
122 Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu
123             165                 170                 175
125 TCT CAA GGT CTG AGG TAC GAA GAA GAC AAA AAG GAG TTG GTG GTA GAC      631
126 Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp
127         180                 185                 190
129 AGT CCC GGG CTC TAC TAC GTA TTT TTG GAA CTG AAG CTC AGT CCA ACA      679
130 Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr
131         195                 200                 205
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133 TTC ACA AAC ACA GGC CAC AAG GTG CAG GGC TGG GTC TCT CTT GTT TTG        727
134 Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu
135 210             215             220             225
137 CAA GCA AAG CCT CAG GTA GAT GAC TTT GAC AAC TTG GCC CTG ACA GTG        775
138 Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val
139             230             235             240
141 GAA CTG TTC CCT TGC TCC ATG GAG AAC AAG TTA GTG GAC CGT TCC TGG        823
142 Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp
143             245             250             255
145 AGT CAA CTG TTG CTC CTG AAG GCT GGC CAC CGC CTC AGT GTG GGT CTG        871
146 Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu
147             260             265             270
149 AGG GCT TAT CTG CAT GGA GCC CAG GAT GCA TAC AGA GAC TGG GAG CTG        919
150 Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu
151             275             280             285
153 TCT TAT CCC AAC ACC ACC AGC TTT GGA CTC TTT CTT GTG AAA CCC GAC        967
154 Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp
155 290             295             300             305
157 AAC CCA TGG GAA TGAGAACTAT CCTTCTTGTG ACTCCTAGTT GCTAAGTCCT          1019
158 Asn Pro Trp Glu
161 CAAGCTGCTA TGTTTTATGG GGTCTGAGCA GGGGTCCCTT CCATGACTTT CTCTTGTCTT    1079
163 TAACTGGACT TGGTATTTAT TCTGAGCATA GCTCAGACAA GACTTTATAT AATTCACTAG    1139
165 ATAGCATTAG TAAACTGCTG GGCAGCTGCT AGATAAAAAA AAATTTCTAA ATCAAAGTTT    1199
167 ATATTTATAT TAATATATAA AAATAAATGT GTTTGTAAAT AAAAAAAAAA AAAAA         1254
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170 (2) INFORMATION FOR SEQ ID NO: 2:

172   (i) SEQUENCE CHARACTERISTICS:

173   (A) LENGTH: 309 amino acids

174   (B) TYPE: amino acid

175   (D) TOPOLOGY: linear

177   (ii) MOLECULE TYPE: protein

179   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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181 Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His
182 1               5               10              15
184 Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr
185             20              25              30
187 Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr
188             35              40              45
190 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg
191 50              55              60
193 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His
194 65              70              75              80
196 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala
197             85              90              95
199 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr
200             100             105             110
202 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln
203             115             120             125
205 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly
206 130             135             140
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208 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys
209 145               150               155               160
211 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr
212               165               170               175
214 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val
215               180               185               190
217 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro
218               195               200               205
220 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val
221       210               215               220
223 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr
224 225               230               235               240
226 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser
227               245               250               255
229 Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly
230               260               265               270
232 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu
233               275               280               285
235 Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro
236       290               295               300
238 Asp Asn Pro Trp Glu
239 305
241 (2) INFORMATION FOR SEQ ID NO: 3:
243       (i) SEQUENCE CHARACTERISTICS:
244             (A) LENGTH: 1618 base pairs
245             (B) TYPE: nucleic acid
246             (C) STRANDEDNESS: single
247             (D) TOPOLOGY: linear
249      (ii) MOLECULE TYPE: cDNA to mRNA
251     (iii) HYPOTHETICAL: NO
253      (iv) ANTI-SENSE: NO
256     (vii) IMMEDIATE SOURCE:
257             (B) CLONE: human 4-1BB-L(7A)
259      (ix) FEATURE:
260             (A) NAME/KEY: CDS
261             (B) LOCATION: 4..765
264      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
266 GTC ATG GAA TAC GCC TCT GAC GCT TCA CTG GAC CCC GAA GCC CCG TGG      48
267     Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp
268     1               5               10               15
270 CCT CCC GCG CCC CGC GCT CGC GCC TGC CGC GTA CTG CCT TGG GCC CTG      96
271 Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu
272               20               25               30
274 GTC GCG GGG CTG CTG CTG CTG CTG CTC GCT GCC GCC TGC GCC GTC      144
275 Val Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val
276               35               40               45
278 TTC CTC GCC TGC CCC TGG GCC GTG TCC GGG GCT CGC GCC TCG CCC GGC      192
279 Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly
280       50               55               60
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Input Set : **N:\Crf3\RULE60\08910449.RAW**
Output Set: **N:\CRF4\07172006\H910449.raw**

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282 TCC GCG GCC AGC CCG AGA CTC CGC GAG GGT CCC GAG CTT TCG CCC GAC      240
283 Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp
284      65             .              70                 75
286 GAT CCC GCC GGC CTC TTG GAC CTG CGG CAG GGC ATG TTT GCG CAG CTG      288
287 Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu
288  80                        85                 90                 95
290 GTG GCC CAA AAT GTT CTG CTG ATC GAT GGG CCC CTG AGC TGG TAC AGT      336
291 Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser
292                    100                105                110
294 GAC CCA GGC CTG GCA GGC GTG TCC CTG ACG GGG GGC CTG AGC TAC AAA      384
295 Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys
296                 115                120                125
298 GAG GAC ACG AAG GAG CTG GTG GTG GCC AAG GCT GGA GTC TAC TAT GTC      432
299 Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val
300             130                135                140
302 TTC TTT CAA CTA GAG CTG CGG CGC GTG GTG GCC GGC GAG GGC TCA GGC      480
303 Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly
304      145                150                155
306 TCC GTT TCA CTT GCG CTG CAC CTG CAG CCA CTG CGC TCT GCT GCT GGG      528
307 Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly
308 160                165                170                175
310 GCC GCC GCC CTG GCT TTG ACC GTG GAC CTG CCA CCC GCC TCC TCC GAG      576
311 Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu
312                 180                185                190
314 GCT CGG AAC TCG GCC TTC GGT TTC CAG GGC CGC TTG CTG CAC CTG AGT      624
315 Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser
316                 195                200                205
318 GCC GGC CAG CGC CTG GGC GTC CAT CTT CAC ACT GAG GCC AGG GCA CGC      672
319 Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg
320                 210                215                220
322 CAT GCC TGG CAG CTT ACC CAG GGC GCC ACA GTC TTG GGA CTC TTC CGG      720
323 His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg
324      225                230                235
326 GTG ACC CCC GAA ATC CCA GCC GGA CTC CCT TCA CCG AGG TCG GAA          765
327 Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
328 240                245                250
330 AACGCCCAGC CTGGGTGCAG CCCACCTGGA CAGAGTCCGA ATCCTACTCC ATCCTTCATG     825
332 GAGACCCCTG GTGCTGGGTC CCTGCTGCTT TCTCTACCTC AAGGGGCTTG GCAGGGGTCC     885
334 CTGCTGCTGA CCTCCCCTTG AGGACCCTCC TCACCCACTC CTTCCCCAAG TTGGACCTTG     945
336 ATATTTATTC TGAGCCTGAG CTCAGATAAT ATATTATATA TATTATATAT ATATATATAT    1005
338 TTCTATTTAA AGAGGATCCT GAGTTTGTGA ATGGACTTTT TTAGAGGAGT TGTTTTGGGG    1065
340 GGGGGGTCTT CGACATTGCC GAGGATTCATC CTTTCTATTA ATTCATTGTA CTTATTTGCC   1125
342 CCTCAGCCTC CCAAGCAACT GGGATTCATC CTTTCTATTA ATTCATTGTA CTTATTTGCC    1185
344 TATTTGTGTG TATTGAGCAT CTGTAATGTG CCAGCATTGT GCCCAGGCTA GGGGGCTATA    1245
346 GAAACATCTA GAAATAGACT GAAAGAAAAT CTGAGTTATG GTAATACGTG AGGAATTTAA    1305
348 AGACTCATCC CCAGCCTCCA CCTCCTGTGT GATACTTGGG GGCTAGCTTT TTTCTTTCTT    1365
350 TCTTTTTTTT GAGATGGTCT TGTTCTGTCA ACCAGGCTAG AATGCAGCGG TGCAATCATG    1425
352 AGTCAATGCA GCCTCCAGCC TCGACCTCCC GAGGCTCAGG TGATCCTCCC ATCTCAGCCT    1485
354 CTCGAGTAGC TGGGACCACA GTTGTGTGCC ACCACACTTG GCTAACTTTT TAATTTTTTT    1545
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/08/910,449**

DATE: 07/18/2006
TIME: 10:52:34

Input Set : **N:\Crf3\RULE60\08910449.RAW**
Output Set: **N:\CRF4\07172006\H910449.raw**

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:39 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)